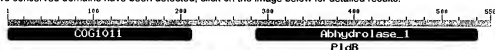


BLAST Basic Local Alignment Search Tool

Job Title: human soluble epoxide hydrolase BLAST

Show Conserved Domains

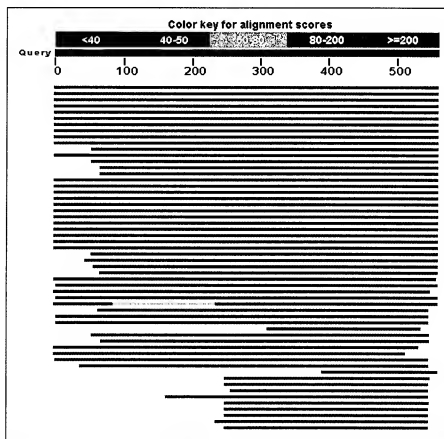
Putative conserved domains have been detected, click on the image below for detailed results.



BLASTP 2.2.18 (Mar-02-2008)

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402. Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109. RID: 190BW5CM014 Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects 6,470,629 sequences; 2,208,486,882 total letters

Query= Length=556

Distribution of 101 Blast Hits on the Query Sequence

Distance (tree) results NEW		Score	
Sequences producing significant alignments:		(Bits)	Value
gb AA011498.1 AK111498.1	soluble epoxide hydrolase [Homo sapiens]	1154	0.0
gb AA011498.1 AK111498.1	Homo sapiens epoxide hydrolase 2, cytoplasmic ...	1154	0.0
gb AA011498.1 AK111498.1	epoxide hydrolase 2, cytoplasmic [Homo sapiens]	1156	0.0
gb AA011498.1 AK111498.1	soluble epoxide hydrolase [Homo sapiens]	1159	0.0
ref XP_001163779.1	PREDICTED: epoxide hydrolase 2, cytoplasmic ...	1163	0.0
gb AA011498.1 AK111498.1	epoxide hydrolase 2, cytoplasmic, isoform CRA_...	1169	0.0
gb AA011498.1 AK111498.1	cytosolic epoxide hydrolase	1169	0.0
ref XP_001163779.1	PREDICTED: epoxide hydrolase 2, cytoplasmic ...	1170	0.0
ref XP_001163779.1	PREDICTED: similar to epoxide hydrolase 2...	1183	0.0
ref XP_001163779.1	PREDICTED: epoxide hydrolase 2, cytoplasmic ...	1195	0.0
gb AA011498.1 AK111498.1	epoxide hydrolase 2, cytoplasmic, isoform CRA_...	1195	0.0
ref XP_001163779.1	PREDICTED: epoxide hydrolase 2, cytoplasmic ...	1199	0.0
gb XP_001163779.1	PREDICTED: epoxide hydrolase 2, cytoplasmic ...	1199	0.0
gb XP_001163779.1	PREDICTED: epoxide hydrolase 2, cytoplasmic ...	1199	0.0
gb XP_001163779.1	PREDICTED: epoxide hydrolase 2, cytoplasmic ...	1199	0.0
ref XP_001163779.1	PREDICTED: similar to epoxide hydrolase 2, c...	1211	0.0
ref XP_001163779.1	PREDICTED: similar to epoxide hydrolase 2, c...	1216	0.0
ref XP_001163779.1	PREDICTED: similar to soluble epoxide hyd...	1220	0.0
ref XP_001163779.1	soluble epoxide hydrolase [Sus scrofa] >...	1224	0.0
ref XP_001163779.1	PREDICTED: similar to epoxide hydrolase 2, c...	1319	0.0
ref XP_001163779.1	PREDICTED: similar to epoxide hydrolase 2, c...	1322	0.0
ref XP_001163779.1	epoxide hydrolase 2, cytoplasmic [Bos tau...	1322	0.0
emb CA065471.1	Epoxide Hydrolase [Mus musculus]	877	0.0
ref NP_031956.2	epoxide hydrolase 2, cytoplasmic [Mus muscul...	878	0.0
gb AA011498.1 AK111498.1	unnamed protein product [Mus musculus]	879	0.0
ref XP_001163779.1	epoxide hydrolase 2, cytoplasmic [Rattus nor...	977	0.0
gb AA011498.1 AK111498.1	Epoxide hydrolase 2, cytoplasmic [Rattus norve...	985	0.0
gb AA011498.1 AK111498.1	epoxide hydrolase 2, cytoplasmic, isoform CRA_...	614	0.0
gb AA011498.1 AK111498.1	epoxide hydrolase 2, cytoplasmic, isoform CRA_...	611	0.0
gb AA011498.1 AK111498.1	ovary-selective epoxide hydrolase [Mus musculus]	603	0.0
gb AA011498.1 AK111498.1	epoxide hydrolase 2C [Mus musculus]	751	0.0
ref XP_001163779.1	PREDICTED: similar to soluble epoxide hyd...	717	0.0
ref XP_001163779.1	epoxide hydrolase 2, cytoplasmic [Xenopus...	677	0.0
ref XP_001163779.1	epoxide hydrolase 2, cytoplasmic [Gallus ...	676	0.0
ref XP_001163779.1	epoxide hydrolase 2, cytoplasmic [Xenopus...	667	0.0
emb CA065471.1	hypothetical protein [Pongo pygmaeus]	644	0.0
ref XP_001163779.1	PREDICTED: similar to epoxide hydrolase 2...	612	3e-173
ref NP_001098642.1	epoxide hydrolase 2, cytoplasmic [Danio r...	572	2e-161
emb CA065471.1	unnamed protein product [Tetraodon nigroviridis]	478	4e-133
gb AA011498.1 AK111498.1	epoxide hydrolase 2, cytoplasmic, isoform CRA_...	463	1e-128
ref XP_001163779.1	PREDICTED: similar to Ephx2-prov protein [St...	454	8e-126
ref XP_001163779.1	PREDICTED: similar to Ephx2-prov protein ...	449	3e-124
ref XP_001163779.1	PREDICTED: similar to Ephx2-prov protein ...	420	1e-115
ref XP_001163779.1	PREDICTED: similar to Ephx2-prov protein, pa...	420	2e-115
ref XP_001163779.1	predicted protein [Nematostella vectensis...	464	1e-110
ref XP_001163779.1	PREDICTED: similar to soluble epoxide hyd...	369	4e-82
ref XP_001163779.1	PREDICTED: hypothetical protein [Bos taurus]	284	1e-74
ref NP_061754.1	epoxide hydrolase [Bradyrhizobium japonicum ...	236	4e-60
ref NP_061754.1	Alpha/beta hydrolase [Rhodospseudomonas palu...	225	6e-60
ref NP_061754.1	alpha/beta hydrolase fold [Parvivaculum l...	234	1e-59
ref XP_001163779.1	PREDICTED: similar to soluble epoxide hyd...	234	1e-59
ref NP_061754.1	epoxide hydrolase [Caulobacter crescentus CB...	222	5e-59
ref NP_061754.1	alpha/beta hydrolase fold [Caulobacter sp...	222	1e-58
ref NP_061754.1	putative epoxide hydrolase [Hyphomonas neptu...	222	2e-57
ref NP_061754.1	epoxide hydrolase [Streptomyces avermitilis ...	223	3e-56
ref NP_061754.1	alpha/beta hydrolase fold [Rhodospseudomonas ...	222	4e-56

ref NP_050280.1	epoxide hydrolase 2, cytoplasmic, isoform CRA...	217	4e-56	G
ref NM_017875.1	PROBABLE EPOXIDE HYDROLASE EPHA (EPOXIDE HYD...	218	7e-56	G
ref AF040712.964.1	alpha/beta hydrolase fold [Clostridium be...	219	3e-55	G
ref AF040712.964.1	epoxide hydrolase Epha [Mycobacterium mar...	218	8e-55	G
ref AF040712.964.1	epoxide hydrolase Epha [Mycobacterium ulcera...	218	8e-55	G
ref AF040712.964.1	epoxide hydrolase [Bradyrhizobium japonicum ...	218	1e-54	G
ref AF040712.964.1	putative epoxide hydrolase [Myxococcus xanth...	217	2e-54	G
ref NP_050280.1	Epha [Mycobacterium avium subsp. paratubercu...	217	2e-54	G
ref AF040712.964.1	COG0596: Predicted hydrolases or acyltrans...	216	3e-54	
ref AF040712.964.1	alpha/beta hydrolase fold [Rhodopseudomonas...	216	4e-54	
ref NP_050280.1	epoxide hydrolase [Agrobacterium tumefaciens...	216	5e-54	G
ref AF040712.964.1	hydrolase, alpha/beta fold family protein [M...	216	6e-54	G
ref NP_050280.1	epoxide hydrolase [Streptomyces coelicolor A...	215	9e-54	G
ref AF040712.964.1	Probable epoxide hydrolase Epha [Mycobact...	214	1e-53	G
ref AF040712.964.1	Putative epoxide hydrolase [Bradyrhizobi...	214	1e-53	G
ref AF040712.964.1	epoxide hydrolase [Rhodopseudomonas palustr...	214	2e-53	G
ref AF040712.964.1	putative epoxide hydrolase [Bradyrhizobi...	213	3e-53	G
ref NP_050280.1	epoxide hydrolase [Agrobacterium tumefaciens...	213	4e-53	G
ref AF040712.964.1	putative epoxide hydrolase [Streptomyces rimo...	209	3e-52	
ref AF040712.964.1	putative epoxide hydrolase [Erythrobacter ...	209	4e-52	
ref AF040712.964.1	putative epoxide hydrolase [Bradyrhizobi...	209	4e-52	G
ref AF040712.964.1	probable epha protein-Mycobacterium tuberc...	209	6e-52	
ref AF040712.964.1	alpha/beta hydrolase fold [Rhodopseudomonas ...	204	2e-50	G
ref AF040712.964.1	unknown [Picea sitchensis]	202	3e-50	
ref NP_050280.1	epoxide hydrolase [Bradyrhizobium japonicum ...	202	6e-50	G
ref CA044344.1	unnamed protein product [Vitis vinifera]	201	9e-50	
ref AF040712.964.1	alpha/beta hydrolase fold [Burkholderia ph...	200	2e-49	
ref AF040712.964.1	epoxide hydrolase [marine gamma proteobact...	200	2e-49	
ref AF040712.964.1	hydrolase, alpha/beta fold family [Alcanivor...	199	4e-49	G
ref AF040712.964.1	alpha/beta hydrolase fold [Rhodopseudomonas ...	199	4e-49	G
ref AF040712.964.1	epoxide hydrolase [Pseudomonas fluorescens Pf-5]	194	5e-49	G
ref AF040712.964.1	epoxide hydrolase [Bradyrhizobium sp. ORS...	199	6e-49	G
ref AF040712.964.1	putative epoxide hydrolase [uncultured marine ...	199	7e-49	
ref NP_050280.1	epoxide hydrolase [Streptomyces avermitilis ...	199	7e-49	G
ref AF040712.964.1	probable epoxide hydrolase [Rhodococcus sp. ...	199	9e-49	G
ref AF040712.964.1	epoxide hydrolase [Mycobacterium smegmatis s...	198	1e-48	G
ref AF040712.964.1	soluble epoxide hydrolase [Citrus jambhiri]	198	1e-48	
ref NP_050280.1	epoxide hydrolase [Streptomyces avermitilis ...	197	1e-48	G
ref AF040712.964.1	alpha/beta hydrolase fold [Mycobacterium ...	197	2e-48	G
ref AF040712.964.1	alpha/beta hydrolase fold [Caulobacter sp...	196	3e-48	G
ref AF040712.964.1	alpha/beta hydrolase fold [Mycobacterium sp...	196	4e-48	G
ref AF040712.964.1	epoxide hydrolase	195	8e-48	
ref AF040712.964.1	Epoxide hydrolase [Medicago truncatula]	194	2e-47	
ref AF040712.964.1	epoxide hydrolase [uncultured marine bacteriu...	194	2e-47	

Alignments

```

>gb|AA014968.1|AF233336_1 G soluble epoxide hydrolase [Homo sapiens]
length=556

GENE ID: 2053 EPHX2 | epoxide hydrolase 2, cytoplasmic [Homo sapiens]
(Over 10 PubMed links)

Score = 1157 bits (2994), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 556/556 (100%), Positives = 556/556 (100%), Gaps = 0/556 (0%)

Query 1 MTLRAAVFDLDGVLALPAVFGVLGRTEALALPGLINDAFQKGQEGGATTRLMKGFTTL 60
      1 MTLRAAVFDLDGVLALPAVFGVLGRTEALALPGLINDAFQKGQEGGATTRLMKGFTTL 60
      1 MTLRAAVFDLDGVLALPAVFGVLGRTEALALPGLINDAFQKGQEGGATTRLMKGFTTL 60

Query 61 SQWIPMEENCRCCKSETAKVCLPKNFSEIKFIPKAI SARKINRPMQLQAALMLRKGFTTTA 120
      1 SQWIPMEENCRCCKSETAKVCLPKNFSEIKFIPKAI SARKINRPMQLQAALMLRKGFTTTA 120
      1 SQWIPMEENCRCCKSETAKVCLPKNFSEIKFIPKAI SARKINRPMQLQAALMLRKGFTTTA 120

Query 121 ILTNTWLDDRAERDGLAQLMCELKMHFDPLIESQVGMVKPFEQIYKFLDITLKASFEV 180
      1 ILTNTWLDDRAERDGLAQLMCELKMHFDPLIESQVGMVKPFEQIYKFLDITLKASFEV 180
      1 ILTNTWLDDRAERDGLAQLMCELKMHFDPLIESQVGMVKPFEQIYKFLDITLKASFEV 180

Query 181 VFLDDIGANKLPARDIGMVITLVQDTPTALKELEKVTGQLLNTPAFLPTSCNPSDMSHG 240
      1 VFLDDIGANKLPARDIGMVITLVQDTPTALKELEKVTGQLLNTPAFLPTSCNPSDMSHG 240
      1 VFLDDIGANKLPARDIGMVITLVQDTPTALKELEKVTGQLLNTPAFLPTSCNPSDMSHG 240

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Conserved Domains



NewSearch

PubMed

Nucleotide

Protein

Structure

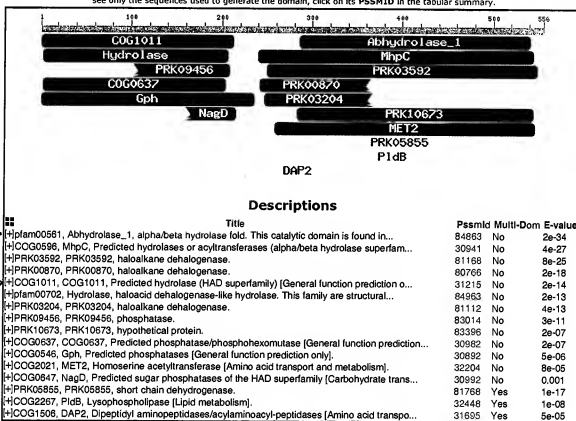
Taxonomy

Help

Query sequence: [(local sequence)|cl|18838]

☐ Concise Result ☒ Full Result ☐ Show Search Information

Click on the **colored bar** for a conserved domain to **view your query sequence** within the multiple sequence alignment for that domain. To see only the sequences used to generate the domain, click on its **PSSMID** in the tabular summary.



Search for similar domain architectures

CD Search Reference:

- [†] Marchler-Bauer A, Bryant SH (2004), "CD-Search: protein domain annotations on the fly.", *Nucleic Acids Res.*32(W)327-331.

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BLAST Basic Local Alignment Search Tool

Job Title: human renin BLAST

Show Conserved Domains

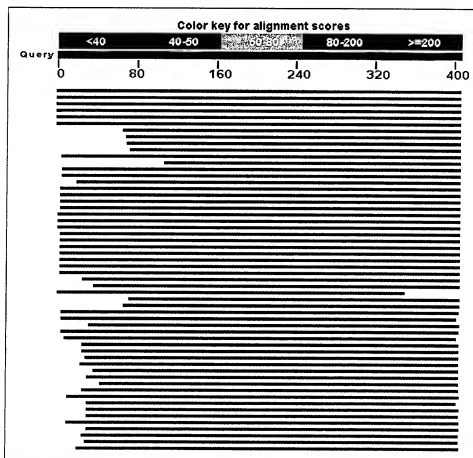
Putative conserved domains have been detected, click on the image below for detailed results.



BLASTP 2.2.18 (Mar-02-2008)

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109. RID: 19U49KAP012
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects 6,470,629 sequences; 2,208,486,882 total letters

Query= Length=406

Distribution of 100 Blast Hits on the Query Sequence

Display: tree of results [NEW](#) [Related Structures](#)

Sequences producing significant alignments:		Score (Bits)	E Value	
ref NP_001002612.1	renin precursor [Homo sapiens] >ref NP_001002612.1	831	0.0	UG
g 12957341 REN1_MACACA	Renin precursor (Angiotensinogenase) >gb...	830	0.0	
ref U01472702.1	renin [Macaca mulatta] >sp Q6DLW5 REN1_MA...	817	0.0	UG
ref U01472702.1	renin [Homo sapiens] >gb EAW91505.1 renin [Ho...	807	0.0	G
g 12957341 REN1_MACACA	Renin precursor (Angiotensinogenase) >em...	803	0.0	G
g 12957341 REN1_MACACA	Renin precursor (Angiotensinogenase) >em...	797	0.0	
g 12957341 REN1_MACACA	Chain A, Crystal Structure Of Renin-PF00074777 Com...	701	0.0	S
g 12957341 REN1_MACACA	Chain A, High Resolution Crystal Structures Of Rec...	696	0.0	S
g 12957341 REN1_MACACA	Chain A, Human ReninPF02342674 COMPLEX >g 12957341 REN1...	694	0.0	S
g 12957341 REN1_MACACA	Chain A, Ketopiperazine-Based Renin Inhibitors: Op...	688	0.0	S
ref U01472702.1	renin [Canis lupus familiaris] >sp Q6DYE7...	621	3e-176	UG
emb CAA44937.1	unnamed protein product [Homo sapiens]	615	3e-174	G
ref NP_001409754.1	PREDICTED: similar to preprorenin [Equus ...	614	3e-174	UG
ref XP_589248.3	PREDICTED: similar to renin [Bos taurus]	612	2e-173	UG
ref NP_001009299.1	renin [Ovis aries] >sp P52115 REN1_SHEEP ...	596	1e-168	UG
ref XP_001472702.1	PREDICTED: similar to renin 2 tandem dupl...	586	1e-165	UG
ref NP_112469.1	renin 1 structural [Mus musculus] >sp P06281...	580	9e-164	UG
g 12957341 REN1_MACACA	renin (Ren-1-d) >g EDL01155.1 MCG129412 [Mus...	579	1e-163	G
ref XP_001472702.1	PREDICTED: similar to renin 2 tandem dupl...	578	2e-163	G
ref NP_001472702.1	renin 1 [Rattus norvegicus] >sp P08424 REN1...	574	4e-162	UG
g 12957341 REN1_MACACA	preprorenin (EC 3.4.99.19)	572	1e-161	G
emb CAA30082.1	unnamed protein product [Rattus norvegicus]	572	2e-161	
g 12957341 REN1_MACACA	synthetic renin 2/1d [Mus musculus]	570	8e-161	
g 12957341 REN1_MACACA	MCG6933 [Mus musculus]	566	1e-159	
sp P00766 REN1_MACACA	Renin-2 precursor (Angiotensinogenase) ...	565	3e-159	G
ref NP_112470.2	renin 2 tandem duplication of Ren1 [Mus musc...	564	4e-159	UG
g 12957341 REN1_MACACA	Ren2 protein [Mus musculus]	563	9e-159	G
g 12957341 REN1_MACACA	renin precursor	560	8e-158	
g 12957341 REN1_MACACA	renin [Mus musculus]	559	1e-157	
emb CAA40050.1	renin [Mus musculus]	544	6e-153	
g 12957341 REN1_MACACA	renin 1, isoform CRA_a [Rattus norvegicus]	526	9e-148	G
g 12957341 REN1_MACACA	renin	490	6e-137	S
g 12957341 REN1_MACACA	Chain A, The 3-D Structure Of Mouse Submaxillary R...	488	2e-136	S
g 12957341 REN1_MACACA	renin	485	3e-135	
ref XP_001370728.1	PREDICTED: similar to preprorenin [Monode...	464	4e-129	UG
emb CA050261.1	renin-like aspartic protease [Echis ocellatus]	446	1e-123	
ref XP_001370728.1	PREDICTED: similar to preprorenin [Ornith...	429	2e-118	UG
ref XP_001370728.1	PREDICTED: similar to preprorenin [Monode...	424	8e-117	
emb CA050260.1	renin-like aspartic protease [Echis ocellatus]	413	1e-113	
ref NP_998025.1	renin [Danio rerio] >g AA031713.1 renin pr...	401	5e-110	UG
g 12957341 REN1_MACACA	renin precursor [Danio rerio] >emb CA013643.1 ...	400	1e-109	
emb CA013643.1	unnamed protein product [Tetraodon nigroviridis]	396	1e-108	
g 12957341 REN1_MACACA	renin [Takifugu rubripes] >tpg DAA01803.1...	395	4e-108	UG
ref XP_001370728.1	PREDICTED: similar to renin [Monodelphis ...	392	1e-107	G
ref XP_001370728.1	PREDICTED: similar to preprorenin [Monode...	382	4e-104	G
ref XP_001370728.1	PREDICTED: similar to preprorenin [Monode...	378	3e-103	
ref NP_965517.1	PREDICTED: similar to CG1548-PA isoform 1 [T...	356	2e-96	UG
ref NP_001072052.1	cathepsin D1 [Takifugu rubripes] >dbj BAD...	355	3e-96	UG
sp Q9D6X3 CATD_CLUHA	Cathepsin D precursor >g AAG27733.1 AF3...	352	4e-95	
ref NP_001085403.1	MGC82347 protein [Xenopus laevis] >g AAH...	352	4e-95	UG
ref NP_001085403.1	cathepsin D preproprotein [Silurus a...	349	2e-94	
g 12957341 REN1_MACACA	Ctsd protein [Danio rerio] >g AAH62824.1 Cts...	349	2e-94	G
g 12957341 REN1_MACACA	cathepsin D precursor [Danio rerio]	349	3e-94	G
ref NP_975746.1	PREDICTED: similar to CG1548-PA isoform 2 [T...	348	4e-94	UG
ref NP_001072052.1	predicted protein [Nematostella vectensis...	347	7e-94	G

ref NP_000772.1	cathepsin D [Lates calcarifer]	347	7e-94	
ref NP_000772.1	PREDICTED: similar to CG1548-PA isoform 3 [T...	347	7e-94	UG
emb CA691476.1	unnamed protein product [Tetraodon nigroviridis]	347	7e-94	
emb CA691476.1	cathepsin D [Danio rerio] >emb CAK05390.1 ca...	347	8e-94	G
ref NP_000772.1	cathepsin D (lysosomal aspartyl protease)...	348	2e-93	UG
ref NP_000772.1	cathepsin D [Gallus gallus] >sp Q05744 CATD_...	348	2e-93	UG
ref NP_000772.1	cathepsin D [Oncorhynchus mykiss]	348	6e-93	G
ref NP_000772.1	cathepsin D [Danio rerio] >emb CAC20111.1 c...	348	4e-92	UG
ref NP_000772.1	PREDICTED: hypothetical protein [Danio re...	348	6e-92	
ref NP_000772.1	cathepsin D; lysosomal aspartic proteinase [Hy...	348	6e-92	
ref NP_000772.1	cathepsin D [Hippoglossus hippoglossus]	348	7e-92	
emb CA691476.1	Cathepsin D [Podarcis sicula]	348	7e-92	
ref NP_000772.1	PREDICTED: cathepsin D isoform 1 [Macaca ...	348	9e-92	UG
ref NP_000772.1	hypothetical protein LOC336746 [Danio rerio]...	348	1e-91	UG
ref NP_000772.1	Unknown (protein for MGC:180677) [Xenopus trop...	348	1e-91	
ref NP_000772.1	LOC613063 protein [Xenopus tropicalis]	348	2e-91	G
ref NP_000772.1	LOC613063 protein [Xenopus tropicalis]	348	2e-91	G
ref NP_000772.1	Cathepsin D precursor	348	3e-91	
ref NP_000772.1	PREDICTED: similar to cathep CG1548-PA [Apis ...	348	4e-91	UG
ref NP_000772.1	AGAP003277-PA [Anopheles gambiae str. PEST] ...	348	4e-91	UG
ref NP_000772.1	hypothetical protein LOC398994 [Xenopus l...	348	5e-91	UG
emb CA691476.1	hypothetical protein [Pongo pygmaeus]	348	7e-91	
ref NP_000772.1	cathepsin D (predicted) [Papio anubis]	348	9e-91	G
ref NP_000772.1	cathepsin D preproprotein (predicted) [Callic...	348	1e-90	
ref NP_000772.1	hypothetical protein LOC443721 [Xenopus l...	348	1e-90	UG
ref NP_000772.1	PREDICTED: cathepsin D isoform 3 [Macaca ...	348	2e-90	UG
ref NP_000772.1	LOC443721 protein [Xenopus laevis]	348	2e-90	G
ref NP_000772.1	unnamed protein product [Macaca fascicularis]	348	3e-90	
ref NP_000772.1	PREDICTED: cathepsin D isoform 2 [Macaca ...	348	3e-90	UG
ref NP_000772.1	cathepsin D (lysosomal aspartyl peptidase) (sy...	348	5e-90	G
ref NP_000772.1	cathepsin D [synthetic construct]	348	7e-90	
ref NP_000772.1	cathepsin D [synthetic construct] >gb AAK42359...	348	7e-90	
ref NP_000772.1	Homo sapiens cathepsin D (lysosomal aspartyl p...	348	8e-90	
ref NP_000772.1	cathepsin D preproprotein [Homo sapiens] >sp...	348	8e-90	UG
ref NP_000772.1	MGC89016 protein [Xenopus tropicalis] >gb...	348	3e-89	UG
ref NP_000772.1	cathepsin D protein [Sus scrofa]	348	4e-89	G
ref NP_000772.1	cathepsin D (predicted) [Rhinolophus ferrumequ...	348	5e-89	
ref NP_000772.1	cathepsin D [Canis lupus familiaris] >sp ...	348	7e-89	UG
emb CA691476.1	cathepsin D precursor [Chionodraco hamatus]	348	1e-88	
ref NP_000772.1	Cathepsin D precursor (Contains: Cathepsin...	348	1e-88	G
ref NP_000772.1	cathepsin D [Rattus norvegicus] >gb AAH62032...	348	2e-88	UG
ref NP_000772.1	cathepsin D (lysosomal aspartyl protease) (X...	348	2e-88	UG
ref NP_000772.1	PREDICTED: similar to GA13759-PA [Nasonia...	348	3e-88	G
ref NP_000772.1	unnamed protein product [Mus musculus]	348	5e-88	UG
ref NP_000772.1	cathepsin D [Sus scrofa] >gb AAK42144.1 ...	348	6e-88	UG

Alignments

```

>ref|NP_000528.1| UG renin precursor (Homo sapiens)
ref|NP_001009122.1| UG renin [Pan troglodytes]
sp|P00797|RENI_HUMAN G Renin precursor (Angiotensinogenase)
sp|P60016|RENI_PANTR G Renin precursor (Angiotensinogenase)
gb|AG30305.1|AF193456.1 G renin [Pan troglodytes]
gb|AAA60363.1| G renin [Homo sapiens]
gb|AAD03461.1| G renin [Homo sapiens]
gb|AAH47752.1| G Renin [Homo sapiens]
emb|CAG38737.1| G Renin [Homo sapiens]
gb|AAH33474.1| G Renin [Homo sapiens]

```



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Descriptions

Title	Pssmid	Multi-Dom	E-value
lplam00026, Asp, Eukaryotic aspartyl protease. Aspartyl (acid) proteases include pepsin...	84452	No	1e-104
lplam07966, A1_Propeptide, A1 Propeptide. Most eukaryotic endopeptidases (Merops Family...	87413	No	0.004

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CD Search Reference:

Marchler-Bauer A, Bryant SH (2004). "CD-Search: protein domain annotations on the fly.", *Nucleic Acids Res.*32(W)327-331.

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